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**Fiber diffraction analysis of cucumber green mottle mosaic virus using limited numbers of heavy-atom derivatives. Erratum.** By SHARON LOBERT and GERALD STUBBS, *Department of Molecular Biology, Vanderbilt University, Nashville, TN 37235, USA*

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**Abstract**

Owing to a printer's error, the left part of Fig. 3(a) of the

paper by Lobert & Stubbs [*Acta Cryst.* (1990), A46, 993–997] was published in the wrong orientation. The correct Fig. 3 is given.

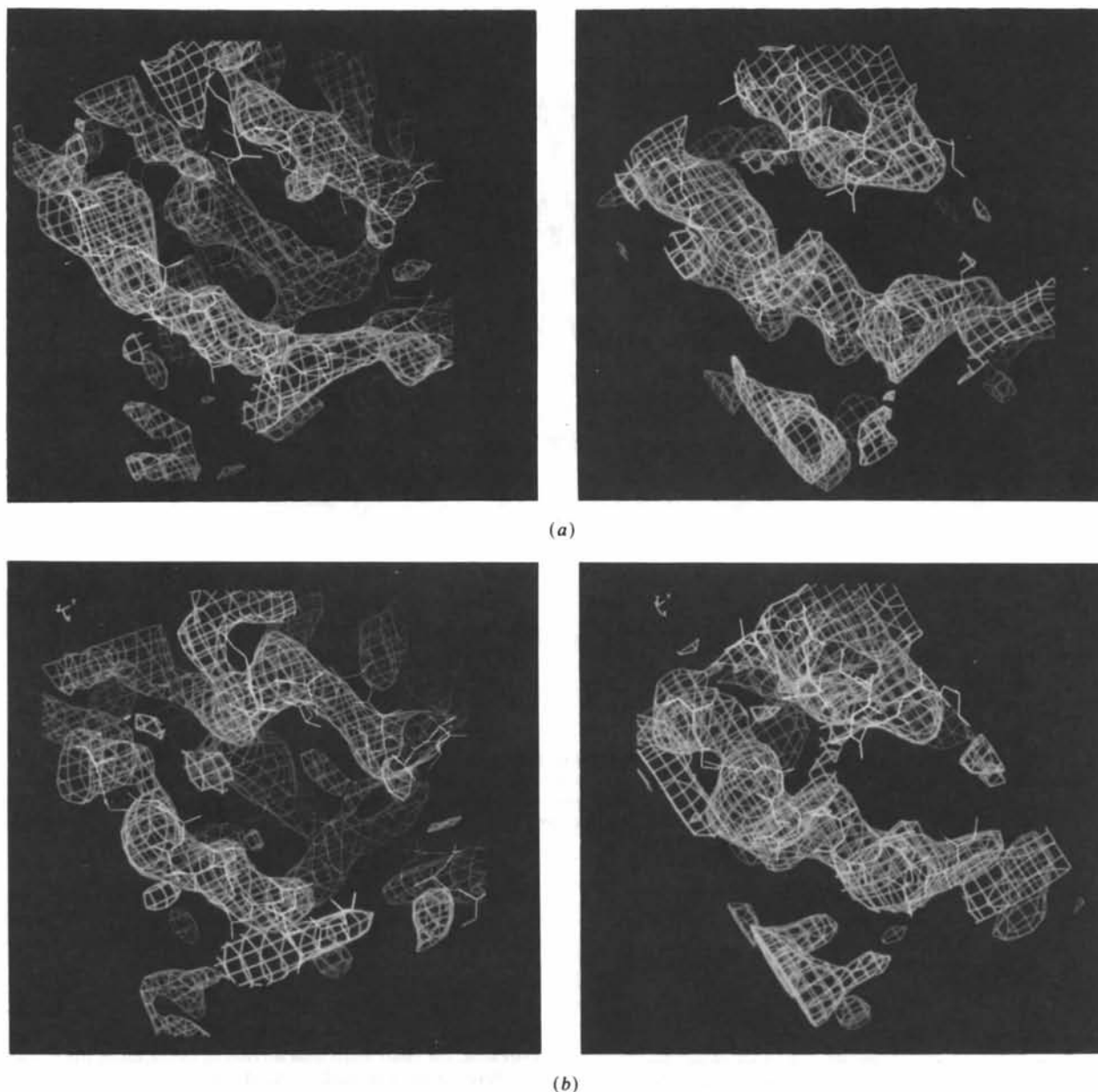


Fig. 3. Electron density maps at 5 Å resolution with the CGMMV-W model superimposed, viewed parallel to the viral axis (looking from the top relative to Fig. 1). The axis is in the top left corner. Three  $\alpha$ -helices are shown in the maps on the left: from top to bottom, RS, RR and LR (see Fig. 1 for helix nomenclature). Two  $\alpha$ -helices are shown in the maps on the right: from top to bottom, RS and LS. (a) Calculated from the initial assumption that all significant amplitudes contributing to an intensity are equal. (b) Calculated from the initial assumption that amplitudes contributing to an intensity have the same relative magnitudes as those calculated from the TMV model.